

SEQUENCE LISTING

<110> Brett P. Monia
Lex M. Cowser

<120> ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION

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Phe Tyr Pro Ala Pro Asp Phe Arg Asp Arg Glu Ala Glu Asp Met Ala

10

15

20

25

gga gtg ttt gac ata gac ctg gac cag cca gag gac gcg ggc tct gag 150

Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu

30

35

40

gat gag ctg gag gag ggg ggt cag tta aat gaa agc atg gac cat ggg 198

Asp Glu Leu Glu Glu Gly Gly Gln Leu Asn Glu Ser Met Asp His Gly

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55

gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa 246

Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu

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70

atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa 294

Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu

75

80

85

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 Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val
 90 95 100 105

ttt caa gta cga aaa gta aca gga gca aat act ggg aaa ata ttt gcc 390
 Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile Phe Ala
 110 115 120

atg aag gtg ctt aaa aag gca atg ata gta aga aat gct aaa gat aca 438
 Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys Asp Thr
 125 130 135

gct cat aca aaa gca gaa cgg aat att ctg gag gaa gta aag cat ccc 486
 Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys His Pro
 140 145 150

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 Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr
 155 160 165

ctc atc ctt gag tat ctc agt gga gga gaa cta ttt atg cag tta gaa 582
 Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu
 170 175 180 185

aga gag gga ata ttt atg gaa gac act gcc tgc ttt tac ttg gca gaa 630
 Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu
 190 195 200

atc tcc atg gct ttg ggg cat tta cat caa aag ggg atc atc tac aga 678
 Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile Tyr Arg
 205 210 215

gac ctg aag ccg gag aat atc atg ctt aat cac caa ggt cat gtg aaa 726
 Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His Val Lys
 220 225 230

cta aca gac ttt gga cta tgc aaa gaa tct att cat gat gga aca gtc 774
 Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly Thr Val
 235 240 245

aca cac aca ttt tgt gga aca ata gaa tac atg gcc cct gaa atc ttg 822
 Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu
 250 255 260 265

atg aga agt ggc cac aat cgt gct gtg gat tgg tgg agt ttg gga gca 870
 Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala
 270 275 280

tta atg tat gac atg ctg act gga gca ccc cca ttc act ggg gag aat 918
 Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly Glu Asn
 285 290 295

aga aag aaa aca att gac aaa atc ctc aaa tgt aaa ctc aat ttg cct 966
 Arg Lys Lys Thr Ile Asp Lys Ile Leu Lys Cys Lys Leu Asn Leu Pro
 300 305 310

ccc tac ctc aca caa gaa gcc aga gat ctg ctt aaa aag ctg ctg aaa 1014
 Pro Tyr Leu Thr Gln Glu Ala Arg Asp Leu Leu Lys Lys Leu Leu Lys
 315 320 325

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Phe Ser Phe Glu Pro Lys Ile Arg Ser Pro Arg Arg Phe Ile Gly Ser			
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Pro Arg Thr Pro Val Ser Pro Val Lys Phe Ser Pro Gly Asp Phe Trp			
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Tyr Pro Met Glu Thr Ser Gly Ile Glu Gln Met Asp Val Thr Met Ser			
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Gly Glu Ala Ser Ala Pro Leu Pro Ile Arg Gln Pro Asn Ser Gly Pro			
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Arg Met Asn Leu			
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